

WHAT IS CLAIMED IS:

1       1. An isolated polynucleotide molecule comprising  
2       an operably linked transcriptional promoter, a polynucleotide  
3       sequence encoding a PIV genome or antigenome, and a  
4       transcriptional terminator, wherein said polynucleotide  
5       sequence encoding said PIV genome or antigenome is modified by  
6       introduction of a heterologous PIV sequence selected from a  
7       HPIV1 sequence, a HPIV2 sequence, a HPIV3 sequence, a BPIV  
8       sequence or a MPIV sequence to form a chimeric PIV genome or  
9       antigenome.

1       2. The isolated polynucleotide molecule of claim  
2       1, wherein a gene or gene segment of human PIV3 is replaced  
3       with a counterpart gene or gene segment from a heterologous  
4       PIV.

1       3. The isolated polynucleotide molecule of claim  
2       2, wherein the counterpart gene or gene segment is a HN or F  
3       glycoprotein gene or gene segment of HPIV1 or HPIV2.

1       4. The isolated polynucleotide molecule of claim  
2       2, wherein an HN or F glycoprotein gene of PIV1 or PIV2 is  
3       substituted for the counterpart HN or F glycoprotein gene of  
4       HPIV3.

1       5. The isolated polynucleotide molecule of claim  
2       1, wherein the polynucleotide sequence encoding the genome or  
3       antigenome incorporates a BPIV gene or gene segment.

1       6. The isolated polynucleotide molecule of claim  
2       1, which incorporates a heterologous sequence from RSV.

1       7. The isolated polynucleotide molecule of claim  
2       6, wherein the heterologous sequence from RSV is a G or F gene  
3       or gene segment.

1               8. The isolated polynucleotide molecule of claim  
2       1, which incorporates a heterologous sequence from measles  
3       virus.

1               9. The isolated polynucleotide molecule of claim  
2       8, wherein the heterologous sequence from measles virus is a  
3       HA or F gene or gene segment.

1               10. An isolated polynucleotide molecule comprising  
2       an operably linked transcriptional promoter, a polynucleotide  
3       sequence encoding a PIV genome or antigenome, and a  
4       transcriptional terminator, wherein said polynucleotide  
5       sequence encoding said PIV genome or antigenome is selected  
6       from the group consisting of:

- 7               i) p218(131) (SEQ ID NO: 1);
- 8               ii) p3/7(131) (SEQ ID NO: 14);
- 9               iii) p3/7(131)2G (SEQ ID NO: 15); or
- 10              iv) the isolated polynucleotide of i), ii) or iii)  
11       modified by introduction of a heterologous PIV sequence  
12       selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV  
13       sequence or a MPIV sequence or by a nucleotide insertion,  
14       rearrangement, deletion or substitution specifying a  
15       phenotypic alteration selected from attenuation, temperature-  
16       sensitivity, cold-adaptation, small plaque size, host range  
17       restriction, or a change in an immunogenic epitope of PIV.

1               11. An isolated polynucleotide molecule comprising  
2       an operably linked transcriptional promoter, a polynucleotide  
3       sequence encoding a PIV genome or antigenome, and a  
4       transcriptional terminator, wherein said polynucleotide  
5       sequence encoding said PIV genome or antigenome is modified by  
6       a nucleotide insertion, rearrangement, deletion or  
7       substitution.

1               12. The isolated polynucleotide molecule of claim  
2       11, wherein said nucleotide insertion, rearrangement, deletion  
3       or substitution specifies a phenotypic alteration selected  
4       from attenuation, temperature-sensitivity, cold-adaptation,

1 small plaque size, host range restriction, or a change in an  
2 immunogenic epitope of PIV.

1 13. The isolated polynucleotide molecule of claim  
2 12, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome incorporates multiple *ts* mutations.

1 14. The isolated polynucleotide molecule of claim  
2 12, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome incorporates multiple non-*ts* attenuating  
4 mutations.

1 15. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome incorporates one or more mutations of JS  
4 *cp45*.

1 16. The isolated polynucleotide molecule of claim  
2 15, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome encodes at least one amino acid  
4 substitution in the polymerase L protein.

1 17. The isolated polynucleotide molecule of claim  
2 16, wherein the amino acid substitution in the polymerase L  
3 protein occurs at a position corresponding to  $\text{Tyr}_{942}$ ,  $\text{Leu}_{992}$ , or  
4  $\text{Thr}_{1558}$  of JS *cp45*.

1 18. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome encodes at least one amino acid  
4 substitution in the N protein.

1 19. The isolated polynucleotide molecule of claim  
2 28, wherein the amino acid substitution in the N protein  
3 occurs at a position corresponding to residues  $\text{Val}_{96}$  or  $\text{Ser}_{389}$   
4 of JS *cp45*.

1           20. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome encodes an amino acid substitution in the  
4 C protein.

1           21. The isolated polynucleotide molecule of claim  
2 20, wherein the amino acid substitution in the C protein  
3 occurs at a position corresponding to Ile<sub>96</sub> of JS cp45.

1           22. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome encodes at least one amino acid  
4 substitution in the F protein.

1           23. The isolated polynucleotide molecule of claim  
2 22, wherein the amino acid substitution in the F protein  
3 occurs at a position corresponding to Ile<sub>420</sub> or Ala<sub>450</sub> of JS  
4 cp45.

1           24. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome encodes an amino acid substitution in the  
4 HN protein.

1           25. The isolated polynucleotide molecule of claim  
2 24, wherein the amino acid substitution in the HN protein  
3 occurs at a position corresponding to residue Val<sub>384</sub> of JS  
4 cp45.

1           26. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome incorporates at least one mutation in a  
4 3' leader sequence.

1           27. The isolated polynucleotide molecule of claim  
2 26, wherein the mutation in the 3' leader occurs at a position  
3 corresponding to nucleotide 23, 24, 28, or 45 of JS cp45.

1           28. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome incorporates a mutation in a N gene start  
4 sequence.

1           29. The isolated polynucleotide molecule of claim  
2 28, wherein the mutation in the N gene start sequence occurs  
3 at a position corresponding to nucleotide 62 of JS cp45.

1           30. The isolated polynucleotide molecule of claim  
2 12, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome incorporates a plurality and up to a full  
4 complement of mutations present in rcp45, rcp45 3'NCMFHN,  
5 rcp45 3'NL, rcp45 3'N, or rcp45 F.

1           31. The isolated polynucleotide molecule of claim  
2 12, which is an antigenomic cDNA selected from rcp45, rcp45  
3 3'NCMFHN, rcp45 3'NL, rcp45 3'N, rcp45 L, rcp45 F, rcp45 M,  
4 rcp45 HN, or rcp45 C.

1           32. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome incorporates a mutation stabilized by  
4 multiple nucleotide substitutions in a codon specifying the  
5 mutation.

1           33. The isolated polynucleotide molecule of claim  
2 11, wherein said polynucleotide sequence encoding said PIV  
3 genome or antigenome incorporates a heterologous sequence from  
4 HPIV1, HPIV2, HPIV3, BPIV or MPIV to form a chimeric genome or  
5 antigenome.

1           34. The isolated polynucleotide molecule of claim  
2 33, wherein said chimeric genome or antigenome incorporates  
3 one or more *ts* mutations.

1           35. The isolated polynucleotide molecule of claim  
2   33, wherein said chimeric genome or antigenome incorporates  
3 one or more non-*ts* attenuating mutations.

1           36. The isolated polynucleotide molecule of claim  
2   33, wherein said chimeric genome or antigenome incorporates  
3 one or more mutations of JS *cp45*.

1           37. The isolated polynucleotide molecule of claim  
2   36, wherein said one or more mutations of JS *cp45* occur in one  
3 or more PIV proteins selected from L, M, N, C, F, or HN or in  
4 a PIV extragenic sequence selected from a 3' leader or N-gene  
5 start sequence.

1           38. The isolated polynucleotide molecule of claim  
2   33, wherein said chimeric genome or antigenome incorporates  
3 multiple mutations each specifying a phenotype selected from  
4 attenuation, temperature-sensitivity, cold-adaptation, small  
5 plaque size, or host range restriction.

1           39. The isolated polynucleotide molecule of claim  
2   33, wherein said chimeric genome or antigenome incorporates at  
3 least one and up to a full complement of mutations present in  
4 *rcp45*, *rcp45* 3'NCMFHN, *rcp45* 3'NL, *rcp45* 3'N, or *rcp45* F.

1           40. The isolated polynucleotide molecule of claim  
2   33, wherein a mutation specifying a phenotypic alteration  
3 selected from attenuation, temperature-sensitivity, cold-  
4 adaptation, small plaque size, host range restriction, or a  
5 change in an immunogenic epitope of PIV is incorporated in a  
6 chimeric PIV background comprising a genome or antigenome  
7 having one or more PIV3 HN or F glycoprotein genes substituted  
8 by one or more counterpart PIV1 or PIV2 HN and F glycoprotein  
9 genes.

1           41. The isolated polynucleotide molecule of claim  
2   33, wherein the heterologous sequence specifies a phenotypic  
3 alteration selected from attenuation, temperature-sensitivity,

4 cold-adaptation, small plaque size, host range restriction, or  
5 a change in an immunogenic epitope of a chimeric PIV.

1 42. The isolated polynucleotide molecule of claim  
2 11, which incorporates a cis-acting regulatory sequence of  
3 HPIV1, HPIV2, BPIV or MPIV.

1 43. The isolated polynucleotide molecule of claim  
2 11, which incorporates a heterologous sequence from RSV.

1 44. The isolated polynucleotide molecule of claim  
2 43, wherein the heterologous sequence from RSV is a G or F  
3 gene or gene segment.

1 45. The isolated polynucleotide molecule of claim  
2 11, which incorporates a heterologous sequence from measles  
3 virus.

1 46. The isolated polynucleotide molecule of claim  
2 45, wherein the heterologous sequence from measles virus is a  
3 HA or F gene or gene segment.

1 47. The isolated polynucleotide molecule of claim  
2 11, which incorporates a polynucleotide sequence encoding a  
3 non-PIV molecule selected from a cytokine, a T-helper epitope,  
4 a restriction site marker, or a protein of a microbial  
5 pathogen capable of eliciting a protective immune response in  
6 a mammalian host.

1 48. A cell or cell-free composition including an  
2 expression vector which comprises an isolated polynucleotide  
3 molecule encoding a PIV genome or antigenome and an expression  
4 vector which comprises one or more isolated polynucleotide  
5 molecules that encode(s) N, P and L proteins of PIV, whereby  
6 expression of said PIV genome or antigenome and N, P, and L  
7 proteins yields an infectious PIV particle.

1           49. The cell or cell-free composition of claim 48,  
2 wherein the infectious PIV particle is a virus.

1           50. The cell or cell-free composition of claim 48,  
2 wherein the infectious PIV particle is a subviral particle.

1           51. The cell or cell-free composition of claim 48,  
2 wherein the polynucleotide encoding the PIV genome or  
3 antigenome and the one or more polynucleotides encoding N, P  
4 and L proteins of PIV are incorporated within a single vector.

1           52. A method for producing an infectious PIV  
2 particle from one or more isolated polynucleotide molecules  
3 encoding said PIV, comprising:

4           coexpressing in a cell or cell-free system an  
5 expression vector which comprises a polynucleotide molecule  
6 encoding a PIV genome or antigenome and an expression vector  
7 which comprises one or more polynucleotide molecules encoding  
8 N, P and L proteins, thereby producing an infectious PIV  
9 particle.

1           53. The method of claim 52, wherein the PIV genome  
2 or antigenome and the N, P, and L proteins are expressed by  
3 the same expression vector.

1           54. The method of claim 52, wherein the N, P, and L  
2 proteins are encoded on two or three different expression  
3 vectors.

1           55. The method of claim 52, wherein at least one of  
2 the N, P and L proteins is supplied by coinfection with PIV.

1           56. The method of claim 52, wherein the  
2 polynucleotide molecule that encodes the PIV genome or  
3 antigenome is cDNA.

1           57. The method of claim 52, wherein the infectious  
2 PIV particle is a virus.

1           58. The method of claim 52, wherein the infectious  
2 PIV particle is a subviral particle.

1           59. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 is a human, bovine or murine PIV sequence.

1           60. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 encodes the sequence of a wild-type PIV strain.

1           61. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 encodes HPIV3.

1           62. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 incorporates an attenuating mutation from a biologically  
4 derived PIV strain.

1           63. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 incorporates one or more *ts* mutations.

1           64. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 incorporates one or more non-*ts* attenuating mutations.

1           65. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 incorporates at least one mutation of JS *cp45*.

1           66. The method of claim 65, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 incorporates multiple mutations of JS *cp45*.

1           67. The method of claim 65, wherein the mutation of  
2 JS cp45 specifies at least one amino acid substitution in the  
3 polymerase L protein.

1           68. The method of claim 67, wherein the amino acid  
2 substitution in the polymerase L occurs at a position  
3 corresponding to Tyr<sub>942</sub>, Leu<sub>992</sub>, or Thr<sub>1558</sub> of JS cp45.

1           69. The method of claim 65, wherein said mutation  
2 of JS cp45 specifies a change in a PIV protein selected from  
3 L, M, N, C, F, or HN or in a PIV extragenic sequence selected  
4 from a 3' leader or N gene start sequence.

1           70. The method of claim 52, wherein said  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 incorporates a mutation that is stabilized by multiple  
4 nucleotide substitutions in a codon which specifies the  
5 mutation.

1           71. The method of claim 52, wherein said  
2 polynucleotide molecule encoding said PIV genome or antigenome  
3 incorporates a plurality and up to a full complement of  
4 mutations present in rcp45, rcp45 3'NCMFHN, rcp45 3'NL, rcp45  
5 3'N, or rcp45 F.

1           72. The method of claim 69, wherein said  
2 polynucleotide molecule encoding said PIV genome or antigenome  
3 is an antigenomic cDNA selected from rcp45, rcp45 3'NCMFHN,  
4 rcp45 3'NL, rcp45 3'N, rcp45 L, rcp45 F, rcp45 M, rcp45 HN, or  
5 rcp45 C.

1           73. The method of claim 52, wherein said  
2 polynucleotide molecule encoding said PIV genome or antigenome  
3 incorporates a heterologous sequence from HPIV1, HPIV2, HPIV3,  
4 BPIV or MPIV to form a chimeric genome or antigenome.

1           74. The method of claim 73, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome

3 is a chimera of a HPIV3 sequence and a HPIV1, HPIV2, BPIV or  
4 MPIV sequence.

1 75. The method of claim 74, wherein a heterologous  
2 sequence from HPIV1 or HPIV2 encoding a gene or gene segment  
3 of an HN or F glycoprotein is substituted for a corresponding  
4 gene or gene segment of HPIV3.

1 76. The method of claim 73, wherein said chimeric  
2 genome or antigenome incorporates one or more *ts* mutations.

1 77. The method of claim 73, wherein said chimeric  
2 genome or antigenome incorporates one or more non-*ts*  
3 attenuating mutations.

1 78. The method of claim 73, wherein said chimeric  
2 genome or antigenome incorporates one or more mutations of JS  
3 cp45.

1 79. The method of claim 73, wherein said chimeric  
2 genome or antigenome incorporates multiple mutations each  
3 specifying a phenotype selected from attenuation, temperature-  
4 sensitivity, cold-adaptation, small plaque size, or host range  
5 restriction.

1 80. The method of claim 73, wherein a mutation  
2 specifying a phenotypic alteration selected from attenuation,  
3 temperature-sensitivity, cold-adaptation, small plaque size,  
4 host range restriction, or a change in an immunogenic epitope  
5 of PIV is incorporated in a chimeric PIV background comprising  
6 a genome or antigenome having one or more PIV3 HN or F  
7 glycoprotein genes substituted by one or more counterpart PIV1  
8 or PIV2 HN and F glycoprotein genes.

1 81. The method of claim 80, wherein one or more  
2 mutations of JS cp45 are incorporated in a chimeric background  
3 comprising a genome or antigenome having both PIV3 HN and F

4 glycoprotein genes substituted by counterpart PIV1 or PIV2 HN  
5 and F glycoprotein genes.

1 82. The method of claim 81, wherein said one or  
2 more mutations of JS cp45 occur in one or more PIV proteins  
3 selected from L, M, N, C, F, or HN or in a PIV extragenic  
4 sequence selected from a 3' leader or N gene start sequence.

1 83. The method of claim 73, wherein the  
2 heterologous sequence specifies a phenotypic alteration  
3 selected from attenuation, temperature-sensitivity, cold-  
4 adaptation, small plaque size, host range restriction, or a  
5 change in an immunogenic epitope of a chimeric PIV.

1 84. The method of claim 52, wherein said  
2 polynucleotide molecule encoding said PIV genome or antigenome  
3 incorporates a heterologous sequence from RSV.

1 85. The method of claim 84, wherein the  
2 heterologous sequence from RSV is a G or F gene or gene  
3 segment.

1 86. The method of claim 52, wherein said  
2 polynucleotide molecule encoding said PIV genome or antigenome  
3 incorporates a heterologous sequence from measles virus.

1 87. The method of claim 86, wherein the  
2 heterologous sequence from measles virus is a HA or F gene or  
3 gene segment.

1 88. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 is selected from:

- 4 i) p218(131) (SEQ ID NO: 1);
- 5 ii) p3/7(131) (SEQ ID NO: 14);
- 6 iii) p3/7(131)2G (SEQ ID NO: 15); or
- 7 iv) the polynucleotide molecule of i), ii) or iii)  
8 modified by introduction of a heterologous PIV sequence

9 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV  
10 sequence or a MPIV sequence or by a nucleotide insertion,  
11 rearrangement, deletion or substitution specifying a  
12 phenotypic alteration selected from attenuation, temperature-  
13 sensitivity, cold-adaptation, small plaque size, host range  
14 restriction, or a change in an immunogenic epitope of PIV.

1 89. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 is selected from:

- 4 i) p218(131) (SEQ ID NO: 1);
- 5 ii) p3/7(131) (SEQ ID NO: 14);
- 6 iii) p3/7(131)2G (SEQ ID NO: 15); or
- 7 iv) the polynucleotide molecule of i), ii) or iii)

8 modified by introduction of a heterologous PIV sequence  
9 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV  
10 sequence or a MPIV sequence and by a nucleotide insertion,  
11 rearrangement, deletion or substitution different from said  
12 introduction of said heterologous PIV sequence specifying a  
13 phenotypic alteration selected from attenuation, temperature-  
14 sensitivity, cold-adaptation, small plaque size, host range  
15 restriction, or a change in an immunogenic epitope of PIV.

1 90. The method of claim 52, wherein the  
2 polynucleotide molecule encoding the PIV genome or antigenome  
3 is modified to encode a non-PIV molecule selected from a  
4 cytokine, a T-helper epitope, a restriction site marker, or a  
5 protein of a microbial pathogen capable of eliciting a  
6 protective immune response in a mammalian host.

1 91. An isolated infectious PIV particle which  
2 comprises a recombinant PIV genome or antigenome, a N protein,  
3 a P protein, and a L protein.

1 92. The isolated infectious PIV particle of claim  
2 91, which is a subviral particle.

1           93. The isolated infectious PIV particle of claim  
2 91, which is a virus.

1           94. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome  
3 incorporates a heterologous sequence from RSV or measles  
4 virus.

1           95. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome is a  
3 cDNA.

1           96. The isolated infectious PIV particle of claim  
2 91, which is a human PIV.

1           97. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome is a  
3 chimera of heterologous PIV sequences selected from HPIV1,  
4 HPIV2, HPIV3, BPIV, or MPIV sequences.

1           98. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome is  
3 selected from:

- 4           i) p218(131) (SEQ ID NO: 1);
- 5           ii) p3/7(131) (SEQ ID NO: 14);
- 6           iii) p3/7(131)2G (SEQ ID NO: 15); or
- 7           iv) the genome or antigenome of i), ii) or iii)

8 modified by introduction of a heterologous PIV sequence  
9 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV  
10 sequence or a MPIV sequence or by a nucleotide insertion,  
11 rearrangement, deletion or substitution specifying a  
12 phenotypic alteration selected from attenuation, temperature-  
13 sensitivity, cold-adaptation, small plaque size, host range  
14 restriction, or a change in an immunogenic epitope of PIV.

1           99. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome is  
3 selected from:

4                   i) p218(131) (SEQ ID NO: 1);  
5                   ii) p3/7(131) (SEQ ID NO: 14);  
6                   iii) p3/7(131)2G (SEQ ID NO: 15); or  
7                   iv) the genome or antigenome of i), ii) or iii)  
8 modified by introduction of a heterologous PIV sequence  
9 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV  
10 sequence or a MPIV sequence and by a nucleotide insertion,  
11 rearrangement, deletion or substitution different from said  
12 introduction of said heterologous PIV sequence specifying a  
13 phenotypic alteration selected from attenuation, temperature-  
14 sensitivity, cold-adaptation, small plaque size, host range  
15 restriction, or a change in an immunogenic epitope of PIV.

1                   100. The isolated infectious PIV particle of claim  
2 91, wherein the counterpart gene or gene segment is a gene or  
3 gene segment of the HN or F glycoprotein gene of HPIV1 or  
4 HPIV2.

1                   101. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome  
3 incorporates a heterologous sequence from RSV or measles  
4 virus.

1                   102. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome is  
3 modified by a nucleotide insertion, rearrangement, deletion or  
4 substitution encoding a phenotypic alteration selected from  
5 attenuation, temperature-sensitivity, cold-adaptation, small  
6 plaque size, host range restriction, or a change in an  
7 immunogenic epitope of PIV.

1                   103. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome  
3 incorporates multiple *ts* mutations.

1                   104. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome  
3 incorporates multiple non-*ts* attenuating mutations.

1           105. The isolated infectious PIV particle of claim  
2   91, wherein the recombinant PIV genome or antigenome  
3   incorporates at least one mutation of JS cp45.

1           106. The isolated infectious PIV particle of claim  
2   105, wherein the mutation of JS cp45 specifies an amino acid  
3   substitution in the polymerase L protein.

1           107. The isolated infectious PIV particle of claim  
2   97, wherein said chimeric genome or antigenome incorporates  
3   one or more *ts* mutations.

1           108. The isolated infectious PIV particle of claim  
2   97, wherein said chimeric genome or antigenome incorporates  
3   one or more non-*ts* attenuating mutations.

1           109. The isolated infectious PIV particle of claim  
2   97, wherein said chimeric genome or antigenome incorporates  
3   one or more mutations of JS cp45.

1           110. The isolated infectious PIV particle of claim  
2   129, wherein said chimeric genome or antigenome incorporates  
3   multiple mutations each specifying a phenotype selected from  
4   attenuation, temperature-sensitivity, cold-adaptation, small  
5   plaque size, or host range restriction.

1           111. The isolated infectious PIV particle of claim  
2   109, wherein said chimeric genome or antigenome incorporates  
3   at least one and up to a full complement of mutations present  
4   in rcp45, rcp45 3'NCMFHN, rcp45 3'NL, rcp45 3'N, or rcp45 F.

1           112. The isolated infectious PIV particle of claim  
2   91, wherein a mutation specifying a phenotypic alteration  
3   selected from attenuation, temperature-sensitivity, cold-  
4   adaptation, small plaque size, host range restriction, or a  
5   change in an immunogenic epitope of PIV is incorporated in a  
6   chimeric PIV background comprising a genome or antigenome  
7   having one or more PIV3 HN or F glycoprotein genes or gene

8 segments substituted by one or more counterpart PIV1 or PIV2  
9 HN and F glycoprotein genes or gene segments.

1 113. The isolated infectious PIV particle of claim  
2 112, wherein one or more mutations of JS cp45 are incorporated  
3 in said chimeric background.

1 114. The isolated infectious PIV particle of claim  
2 of claim 113, wherein said one or more mutations of JS cp45  
3 occur in one or more PIV proteins selected from L, M, N, C, F,  
4 or HN or in a PIV extragenic sequence selected from a 3'  
5 leader or N gene start sequence.

1 115. The isolated infectious PIV particle of claim  
2 91, wherein the recombinant PIV genome or antigenome is  
3 modified to encode a non-PIV molecule selected from a  
4 cytokine, a T-helper epitope, a restriction site marker, or a  
5 protein of a microbial pathogen capable of eliciting a  
protective immune response in a mammalian host.

1 116. The isolated infectious PIV particle of claim  
2 91, further comprising an RSV antigen or epitope which elicits  
3 protective immunity to RSV in an immunized host.

1 117. The isolated infectious PIV particle of claim  
2 91, which is selected from r942, r992, r1558, r942/992,  
3 r992/1558, r942/1558, or r942/992/1558, rcp45 3'N, rcp45 C,  
4 rcp45 M, rcp45 F, rcp45 HN, rcp45L, rcp45 3'NL, rcp45  
5 3'NCMFHN, and rcp45.

1 118. An immunogenic composition comprising an  
2 immunogenically effective amount of an infectious PIV particle  
3 in a pharmaceutically acceptable carrier, said PIV particle  
4 comprising a recombinant PIV genome or antigenome, a N  
5 protein, a P protein, and a L protein.

1 119. The immunogenic composition of claim 118,  
2 wherein said infectious PIV particle is a subviral particle.

1           120. The immunogenic composition of claim 118,  
2 wherein said infectious PIV particle is a virus.

1           121. The immunogenic composition of claim 118,  
2 wherein the recombinant PIV genome or antigenome incorporates  
3 a heterologous sequence from RSV or measles virus.

1           122. The immunogenic composition of claim 118,  
2 wherein the recombinant PIV genome or antigenome is a chimera  
3 of heterologous PIV sequences selected from HPIV1, HPIV2,  
4 HPIV3, BPIV, or MPIV sequences to form an infectious, chimeric  
5 PIV particle.

1           123. The immunogenic composition of claim 118,  
2 wherein the recombinant PIV genome or antigenome encodes a  
3 human PIV in which a gene or gene segment is replaced with a  
4 counterpart gene or gene segment from a heterologous PIV.

1           124. The immunogenic composition of claim 123,  
2 wherein one or both HN and F glycoprotein genes of HPIV1 are  
3 substituted for HN and F glycoprotein genes of HPIV3 to form  
4 said infectious, chimeric PIV particle.

1           125. The immunogenic composition of claim 123,  
2 wherein the recombinant PIV genome or antigenome of said  
3 infectious, chimeric PIV particle is modified by a nucleotide  
4 insertion, rearrangement, deletion or substitution encoding a  
5 phenotypic alteration selected from attenuation, temperature-  
6 sensitivity, cold-adaptation, small plaque size, host range  
7 restriction, or a change in an immunogenic epitope of PIV.

1           126. The immunogenic composition of claim 125,  
2 wherein said recombinant PIV genome or antigenome incorporates  
3 multiple mutations selected from ts and non-ts attenuating  
4 mutations to form an attenuated, infectious, chimeric PIV  
5 particle.

1           127. The immunogenic composition of claim 118,  
2   wherein the recombinant PIV genome or antigenome incorporates  
3   a mutation of JS *cp45*.

1           128. The immunogenic composition of claim 118,  
2   wherein the recombinant PIV genome or antigenome incorporates  
3   multiple mutations of JS *cp45*.